



SEQUENCE LISTING

<110> NIPPON MEDICAL SCHOOL

<120> Fusion cell death inducing gene specifically acting on
vascularizing endothelial cells

<130> P02-1021

<140>

<141>

<160> 27

<170> PatentIn Ver. 2.1

<210> 1

<211> 579

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(579)

<400> 1

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Met Asp Gly Ser Gly Glu Gln Pro Arg Gly Gly Pro Thr Ser Ser

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10

15

gag cag atc atg aag aca ggg gcc ctt ttg ctt cag ggt ttc atc cag 96

Glu Gln Ile Met Lys Thr Gly Ala Leu Leu Leu Gln Gly Phe Ile Gln

20

25

30

gat cga gca ggg cga atg ggg gag gca ccc gag ctg gcc ctg gac 144

Asp Arg Ala Gly Arg Met Gly Gly Glu Ala Pro Glu Leu Ala Leu Asp

35

40

45

ccg gtg cct cag gat gcg tcc acc aag aag ctg agc gag tgt ctc aag 192

Pro Val Pro Gln Asp Ala Ser Thr Lys Lys Leu Ser Glu Cys Leu Lys

50

55

60

cgc atc ggg gac gaa ctg gac agt aac atg gag ctg cag agg atg att 240

Arg Ile Gly Asp Glu Leu Asp Ser Asn Met Glu Leu Gln Arg Met Ile

65

70

75

80

gcc gcc gtg gac aca gac tcc ccc cga gag gtc ttt ttc cga gtg gca 288

Ala Ala Val Asp Thr Asp Ser Pro Arg Glu Val Phe Phe Arg Val Ala

85

90

95

gct gac atg ttt tct gac ggc aac ttc aac tgg ggc cgg gtt gtc gcc 336

Ala Asp Met Phe Ser Asp Gly Asn Phe Asn Trp Gly Arg Val Val Ala

100

105

110

ctt ttc tac ttt gcc agc aaa ctg gtg ctc aag gcc ctg tgc acc aag 384

Leu Phe Tyr Phe Ala Ser Lys Leu Val Leu Lys Ala Leu Cys Thr Lys

115

120

125

gtg ccg gaa ctg atc aga acc atc atg ggc tgg aca ttg gac ttc ctc 432

Val Pro Glu Leu Ile Arg Thr Ile Met Gly Trp Thr Leu Asp Phe Leu

130

135

140

cgg gag cgg ctg ttg ggc tgg atc caa gac cag ggt ggt tgg gac ggc 480
Arg Glu Arg Leu Leu Gly Trp Ile Gln Asp Gln Gly Gly Trp Asp Gly
145 150 155 160

ctc ctc tcc tac ttt ggg acg ccc acg tgg cag acc gtg acc atc ttt 528
Leu Leu Ser Tyr Phe Gly Thr Pro Thr Trp Gln Thr Val Thr Ile Phe
165 170 175

gtg gcg gga gtg ctc acc gcc tcg ctc acc atc tgg aag aag atg ggc 576
Val Ala Gly Val Leu Thr Ala Ser Leu Thr Ile Trp Lys Lys Met Gly
180 185 190

tga 579

<210> 2

<211> 192

<212> PRT

<213> Homo sapiens

<400> 2

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Glu Gln Ile Met Lys Thr Gly Ala Leu Leu Gln Gly Phe Ile Gln
20 25 30

Asp Arg Ala Gly Arg Met Gly Gly Glu Ala Pro Glu Leu Ala Leu Asp
35 40 45

Pro Val Pro Gln Asp Ala Ser Thr Lys Lys Leu Ser Glu Cys Leu Lys
50 55 60

Arg Ile Gly Asp Glu Leu Asp Ser Asn Met Glu Leu Gln Arg Met Ile
65 70 75 80
Ala Ala Val Asp Thr Asp Ser Pro Arg Glu Val Phe Phe Arg Val Ala
85 90 95
Ala Asp Met Phe Ser Asp Gly Asn Phe Asn Trp Gly Arg Val Val Ala
100 105 110
Leu Phe Tyr Phe Ala Ser Lys Leu Val Leu Lys Ala Leu Cys Thr Lys
115 120 125
Val Pro Glu Leu Ile Arg Thr Ile Met Gly Trp Thr Leu Asp Phe Leu
130 135 140
Arg Glu Arg Leu Leu Gly Trp Ile Gln Asp Gln Gly Gly Trp Asp Gly
145 150 155 160
Leu Leu Ser Tyr Phe Gly Thr Pro Thr Trp Gln Thr Val Thr Ile Phe
165 170 175
Val Ala Gly Val Leu Thr Ala Ser Leu Thr Ile Trp Lys Lys Met Gly
180 185 190

<210> 3

<211> 999

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(999)

<400> 3

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Met Ala Cys Asp Cys Arg Gly Asp Cys Phe Cys Gly Gly Met Ser Lys

1 5 10 15

ggc gag gaa ctg ttc act ggc gtg gtc cca att ctc gtg gaa ctg gat 96

Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp

20 25 30

ggc gat gtg aat ggg cac aaa ttt tct gtc agc gga gag ggt gaa ggt 144

Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly

35 40 45

gat gcc aca tac gga aag ctc acc ctg aaa ttc atc tgc acc act gga 192

Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly

50 55 60

aag ctc cct gtg cca tgg cca aca ctg gtc act acc ttc acc tat ggc 240

Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Thr Tyr Gly

65 70 75 80

gtg cag tgc ttt tcc aga tac cca gac cat atg aag cag cat gac ttt 288

Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe

85 90 95

ttc aag agc gcc atg ccc gag ggc tat gtg cag gag aga acc atc ttt 336

Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe

100 105 110

ttc aaa gat gac ggg aac tac aag acc cgc gct gaa gtc aag ttc gaa 384

Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu

115 120 125

ggt gac acc ctg gtg aat aga atc gag ctg aag ggc att gac ttt aag 432
Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
130 135 140

gag gat gga aac att ctc ggc cac aag ctg gaa tac aac tat aac tcc 480
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
145 150 155 160

cac aat gtg tac atc atg gcc gac aag caa aag aat ggc atc aag gtc 528
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
165 170 175

aac ttc aag atc aga cac aac att gag gat gga tcc gtg cag ctg gcc 576
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
180 185 190

gac cat tat caa cag aac act cca atc ggc gac ggc cct gtg ctc ctc 624
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
195 200 205

cca gac aac cat tac ctg tcc acc cag tct gcc ctg tct aaa gat ccc 672
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
210 215 220

aac gaa aag aga gac cac atg gtc ctg ctg gag ttt gtg acc gct gct 720
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
225 230 235 240

ggg atc aca cat ggc atg gac gag ctg tac aag gcc ctt ttc tac ttt 768

Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Ala Leu Phe Tyr Phe

245

250

255

gcc agc aaa ctg gtg ctc aag gcc ctg tgc acc aag gtg ccg gaa ctg 816

Ala Ser Lys Leu Val Leu Lys Ala Leu Cys Thr Lys Val Pro Glu Leu

260

265

270

atc aga acc atc atg ggc tgg aca ttg gac ttc ctc cgg gag cgg ctg 864

Ile Arg Thr Ile Met Gly Trp Thr Leu Asp Phe Leu Arg Glu Arg Leu

275

280

285

ttg ggc tgg atc caa gac cag ggt ggt tgg gac ggc ctc ctc tcc tac 912

Leu Gly Trp Ile Gln Asp Gln Gly Gly Trp Asp Gly Leu Leu Ser Tyr

290

295

300

ttt ggg acg ccc acg tgg cag acc gtg acc atc ttt gtg gcg gga gtg 960

Phe Gly Thr Pro Thr Trp Gln Thr Val Thr Ile Phe Val Ala Gly Val

305

310

315

320

ctc acc gcc tca ctc acc atc tgg aag aag atg ggc tga 999

Leu Thr Ala Ser Leu Thr Ile Trp Lys Lys Met Gly

325

330

<210> 4

<211> 332

<212> PRT.

<213> Homo sapiens

<400> 4

Met Ala Cys Asp Cys Arg Gly Asp Cys Phe Cys Gly Gly Met Ser Lys

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1 | 5 | 10 | 15 | | | | | | | | | | | | |
| Gly | Glu | Glu | Leu | Phe | Thr | Gly | Val | Val | Pro | Ile | Leu | Val | Glu | Leu | Asp |
| | | | | | | | | | | | | | | | |
| 20 | | 25 | | | | | | | | | | 30 | | | |
| Gly | Asp | Val | Asn | Gly | His | Lys | Phe | Ser | Val | Ser | Gly | Glu | Gly | Glu | Gly |
| | | | | | | | | | | | | | | | |
| 35 | | 40 | | | | | | | | | | 45 | | | |
| Asp | Ala | Thr | Tyr | Gly | Lys | Leu | Thr | Leu | Lys | Phe | Ile | Cys | Thr | Thr | Gly |
| | | | | | | | | | | | | | | | |
| 50 | | 55 | | | | | | | | | 60 | | | | |
| Lys | Leu | Pro | Val | Pro | Trp | Pro | Thr | Leu | Val | Thr | Thr | Phe | Thr | Tyr | Gly |
| | | | | | | | | | | | | | | | |
| 65 | | 70 | | | | | | | 75 | | | 80 | | | |
| Val | Gln | Cys | Phe | Ser | Arg | Tyr | Pro | Asp | His | Met | Lys | Gln | His | Asp | Phe |
| | | | | | | | | | | | | | | | |
| 85 | | | 90 | | | | | | | | | 95 | | | |
| Phe | Lys | Ser | Ala | Met | Pro | Glu | Gly | Tyr | Val | Gln | Glu | Arg | Thr | Ile | Phe |
| | | | | | | | | | | | | | | | |
| 100 | | | 105 | | | | | | | | 110 | | | | |
| Phe | Lys | Asp | Asp | Gly | Asn | Tyr | Lys | Thr | Arg | Ala | Glu | Val | Lys | Phe | Glu |
| | | | | | | | | | | | | | | | |
| 115 | | | 120 | | | | | | | 125 | | | | | |
| Gly | Asp | Thr | Leu | Val | Asn | Arg | Ile | Glu | Leu | Lys | Gly | Ile | Asp | Phe | Lys |
| | | | | | | | | | | | | | | | |
| 130 | | | 135 | | | | | | | 140 | | | | | |
| Glu | Asp | Gly | Asn | Ile | Leu | Gly | His | Lys | Leu | Glu | Tyr | Asn | Tyr | Asn | Ser |
| | | | | | | | | | | | | | | | |
| 145 | | | 150 | | | | | 155 | | | | 160 | | | |
| His | Asn | Val | Tyr | Ile | Met | Ala | Asp | Lys | Gln | Lys | Asn | Gly | Ile | Lys | Val |
| | | | | | | | | | | | | | | | |
| 165 | | | 170 | | | | | | | | | 175 | | | |
| Asn | Phe | Lys | Ile | Arg | His | Asn | Ile | Glu | Asp | Gly | Ser | Val | Gln | Leu | Ala |
| | | | | | | | | | | | | | | | |
| 180 | | | 185 | | | | | | | | 190 | | | | |
| Asp | His | Tyr | Gln | Gln | Asn | Thr | Pro | Ile | Gly | Asp | Gly | Pro | Val | Leu | Leu |
| | | | | | | | | | | | | | | | |
| 195 | | | 200 | | | | | | | | 205 | | | | |
| Pro | Asp | Asn | His | Tyr | Leu | Ser | Thr | Gln | Ser | Ala | Leu | Ser | Lys | Asp | Pro |
| | | | | | | | | | | | | | | | |
| 210 | | | 215 | | | | | | | 220 | | | | | |
| Asn | Glu | Lys | Arg | Asp | His | Met | Val | Leu | Leu | Glu | Phe | Val | Thr | Ala | Ala |
| | | | | | | | | | | | | | | | |
| 225 | | | 230 | | | | | 235 | | | | 240 | | | |
| Gly | Ile | Thr | His | Gly | Met | Asp | Glu | Leu | Tyr | Lys | Ala | Leu | Phe | Tyr | Phe |

| | | |
|---|-----|-----|
| 245 | 250 | 255 |
| Ala Ser Lys Leu Val Leu Lys Ala Leu Cys Thr Lys Val Pro Glu Leu | | |
| 260 | 265 | 270 |
| Ile Arg Thr Ile Met Gly Trp Thr Leu Asp Phe Leu Arg Glu Arg Leu | | |
| 275 | 280 | 285 |
| Leu Gly Trp Ile Gln Asp Gln Gly Gly Trp Asp Gly Leu Leu Ser Tyr | | |
| 290 | 295 | 300 |
| Phe Gly Thr Pro Thr Trp Gln Thr Val Thr Ile Phe Val Ala Gly Val | | |
| 305 | 310 | 315 |
| Leu Thr Ala Ser Leu Thr Ile Trp Lys Lys Met Gly | | |
| 325 | 330 | |

<210> 5

<211> 987

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(987)

<400> 5

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| Met Ala Cys Asn Gly Arg Cys Gly Gly Met Ser Lys Gly Glu Glu Leu | | | |
| 1 | 5 | 10 | 15 |

| | |
|---|----|
| ttc act ggc gtg gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat | 96 |
| Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn | |

| | | | |
|---|-----|-----|-----|
| 20 | 25 | 30 | |
| ggg cac aaa ttt tct gtc agc gga gag ggt gaa ggt gat gcc aca tac | | | 144 |
| Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Asp Ala Thr Tyr | | | |
| 35 | 40 | 45 | |
| gga aag ctc acc ctg aaa ttc atc tgc acc act gga aag ctc cct gtg | | | 192 |
| Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val | | | |
| 50 | 55 | 60 | |
| cca tgg cca aca ctg gtc act acc ttc acc tat ggc gtg cag tgc ttt | | | 240 |
| Pro Trp Pro Thr Leu Val Thr Phe Thr Tyr Gly Val Gln Cys Phe | | | |
| 65 | 70 | 75 | 80 |
| tcc aga tac cca gac cat atg aag cag cat gac ttt ttc aag agc gcc | | | 288 |
| Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala | | | |
| 85 | 90 | 95 | |
| atg ccc gag ggc tat gtg cag gag aga acc atc ttt ttc aaa gat gac | | | 336 |
| Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp | | | |
| 100 | 105 | 110 | |
| ggg aac tac aag acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg | | | 384 |
| Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu | | | |
| 115 | 120 | 125 | |
| gtg aat aga atc gag ctg aag ggc att gac ttt aag gag gat gga aac | | | 432 |
| Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn | | | |
| 130 | 135 | 140 | |
| att ctc ggc cac aag ctg gaa tac aac tat aac tcc cac aat gtg tac | | | 480 |

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
145 150 155 160

atc atg gcc gac aag caa aag aat ggc atc aag gtc aac ttc aag atc 528
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
165 170 175

aga cac aac att gag gat gga tcc gtg cag ctg gcc gac cat tat caa 576
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
180 185 190

cag aac act cca atc ggc gac ggc cct gtg ctc ctc cca gac aac cat 624
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
195 200 205

tac ctg tcc acc cag tct gcc ctg tct aaa gat ccc aac gaa aag aga 672
Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
210 215 220

gac cac atg gtc ctg ctg gag ttt gtg acc gct gct ggg atc aca cat 720
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His
225 230 235 240

ggc atg gac gag ctg tac aag gcc ctt ttc tac ttt gcc agc aaa ctg 768
Gly Met Asp Glu Leu Tyr Lys Ala Leu Phe Tyr Phe Ala Ser Lys Leu
245 250 255

gtg ctc aag gcc ctg tgc acc aag gtg ccg gaa ctg atc aga acc atc 816
Val Leu Lys Ala Leu Cys Thr Lys Val Pro Glu Leu Ile Arg Thr Ile
260 265 270

atg ggc tgg aca ttg gac ttc ctc cg_g gag cg_g ctg ttg ggc tgg atc 864
Met Gly Trp Thr Leu Asp Phe Leu Arg Glu Arg Leu Leu Gly Trp Ile
275 280 285

caa gac cag ggt ggt tgg gac ggc ctc ctc tcc tac ttt ggg acg ccc 912
Gln Asp Gln Gly Gly Trp Asp Gly Leu Leu Ser Tyr Phe Gly Thr Pro
290 295 300

acg tgg cag acc gtg acc atc ttt gtg gc_g gga gtg ctc acc gcc tca 960
Thr Trp Gln Thr Val Thr Ile Phe Val Ala Gly Val Leu Thr Ala Ser
305 310 315 320

ctc acc atc tgg aag aag atg ggc tga 987
Leu Thr Ile Trp Lys Lys Met Gly
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<210> 6

<211> 328

<212> PRT

<213> Homo sapiens

<400> 6

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Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn
20 25 30
Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr
35 40 45

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
50 55 60
Pro Trp Pro Thr Leu Val Thr Thr Phe Thr Tyr Gly Val Gln Cys Phe
65 70 75 80
Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala
85 90 95
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
100 105 110
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
115 120 125
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
130 135 140
Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
145 150 155 160
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
165 170 175
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
180 185 190
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
195 200 205
Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
210 215 220
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His
225 230 235 240
Gly Met Asp Glu Leu Tyr Lys Ala Leu Phe Tyr Phe Ala Ser Lys Leu
245 250 255
Val Leu Lys Ala Leu Cys Thr Lys Val Pro Glu Leu Ile Arg Thr Ile
260 265 270
Met Gly Trp Thr Leu Asp Phe Leu Arg Glu Arg Leu Leu Gly Trp Ile
275 280 285

Gln Asp Gln Gly Gly Trp Asp Gly Leu Leu Ser Tyr Phe Gly Thr Pro
290 295 300
Thr Trp Gln Thr Val Thr Ile Phe Val Ala Gly Val Leu Thr Ala Ser
305 310 315 320
Leu Thr Ile Trp Lys Lys Met Gly
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<210> 7

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Homing peptide

<400> 7

Cys Leu Ser Ser Arg Leu Asp Ala Cys

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<210> 8

<211> 9

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Homing peptide

<400> 8

Cys Asn Ser Arg Leu His Leu Arg Cys

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<210> 9

<211> 9

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Homing peptide

<400> 9

Cys Glu Asn Trp Trp Gly Asp Val Cys

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<210> 10

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Homing peptide

<400> 10

Trp Arg Cys Val Leu Arg Glu Gly Pro Ala Gly Gly Cys Ala Trp Phe

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Asn Arg His Arg Leu

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<210> 11
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Homing peptide

<400> 11
Cys Leu Pro Val Ala Ser Cys
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<210> 12
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
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<400> 12
Cys Gly Ala Arg Glu Met Cys
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<210> 13
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<223> Description of Artificial Sequence:Homing peptide

<400> 13

Cys Lys Ser Thr His Asp Arg Leu Cys

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<210> 14

<211> 9

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Homing peptide

<400> 14

Cys Gly Asn Lys Arg Thr Arg Gly Cys

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<210> 15

<211> 5

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Homing peptide

<400> 15

Ala Pro Arg Pro Gly

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<210> 16

<211> 6

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Homing peptide

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Lys Gln Ala Gly Asp Val

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<210> 17

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Homing peptide

<400> 17

Lys Arg Leu Asp Gly Ser

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<210> 18
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Homing peptide

<400> 18
Asp Gly Glu Ala
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<210> 19
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<220>
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<222> (1)..(2)
<223> n is A, C, G or T

<400> 19
nnatcgatcc accatgagca agggcgag

28

<210> 20

<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 20
ctggcaaagt agaaaagggc cttgtacagc tcgtc 35

<210> 21
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 21
gccctttct actttgccag 20

<210> 22
<211> 26
<212> DNA
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<220>
<223> Description of Artificial Sequence:Primer

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<400> 22

nntctagatc agcccatctt cttcca

26

<210> 23
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<223> Description of Artificial Sequence:Primer

<400> 23

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<210> 24
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<223> Description of Artificial Sequence:Primer

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<400> 24
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<210> 25
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<220>
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<400> 25
tgaaaaagca ctgcacgc 18

<210> 26
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<212> DNA
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<220>
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ccatggcctg caacggtcgt tgcggtgtta tgagcaaggg cgagg 45

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<222> (1)..(4)

<223> n is A, C, G or T

<400> 27

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22